

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 10/536,809  
Source: PCT  
Date Processed by STIC: 6/7/05

# ***ENTERED***

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PCT

## RAW SEQUENCE LISTING

DATE: 06/07/2005

PATENT APPLICATION: US/10/536,809

TIME: 11:17:11

Input Set : A:\08959.0011 Sequence Listing.txt

Output Set: N:\CRF4\06072005\J536809.raw

3 <110> APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.  
 5 <120> TITLE OF INVENTION: Canine CYP1A2 genetic polymorphism  
 7 <130> FILE REFERENCE: Y0414PCT-712  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/536,809  
 C--> 9 <141> CURRENT FILING DATE: 2005-05-27  
 9 <150> PRIOR APPLICATION NUMBER: JP 2003-152917  
 10 <151> PRIOR FILING DATE: 2003-05-29  
 12 <150> PRIOR APPLICATION NUMBER: JP 2003-206581  
 13 <151> PRIOR FILING DATE: 2003-08-07  
 15 <160> NUMBER OF SEQ ID NOS: 23  
 17 <170> SOFTWARE: PatentIn version 3.1  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 1380  
 21 <212> TYPE: DNA  
 22 <213> ORGANISM: Canis familiaris  
 24 <220> FEATURE:  
 25 <223> OTHER INFORMATION: Inventor: Tenmizu, Daisuke; Fukunaga, Yasuhisa; Noguchi,  
 Kiyoshi  
 28 <400> SEQUENCE: 1  
 29 ctggagtctt atgtaccttg tggcaaacc tggagatacag agaaagatcc agaaggagtt 60  
 31 gggatatgcg tagagatgca caagctaaga gaagcttgag atccccagg tctttgttca 120  
 33 atgacatata gctgttgtgt gcctaccatg tgtaagccct gggcatacac tgggtgccac 180  
 35 ccttgccctag aacatgctgg ggtaggggtg ttactgggcc ttagatatat aacagacagt 240  
 37 actatgtaat aggggactta gataccatga agcagtcggg gcagccctaa gcccggtttg 300  
 39 gtcttctgtg ttctgcagac acgggtgatt gcagggcacg gcagcctcgc ctctctgaca 360  
 41 ggccccagct gcccttaatg gaggccttca tcctggagat cttctgacac acctccttta 420  
 43 tccccctcac catccccac aggtaaggcc tgcttcttct gccttgccac ctttgtagcc 480  
 45 ttcacatgt ttcttctctc catcttctca gccctggatc tggctcagac ctcggcctct 540  
 47 cacttctggc cagctcacca agttccccctc agcctcttgg ctgccgacaa ccaatccaac 600  
 49 catgatcaaa ctaccagct ttcaggagaa agtcacactg ctgatctcag ctctcattca 660  
 51 cctctgctca cattccttct ctgcaagtac tctcaatcca cccgggctgg cctcgctgta 720  
 53 cctccccagc atgatgcggt caacctccaa ttttgcttat gctggacctt ctgctggaa 780  
 55 tgccctttta cctcttctcc caccacctga atcttaccct tgcccaaggc caatcctgac 840  
 57 acaaacttcc ccttcaactat caggctttct tgactcatcc agctggcaca gcttcattct 900  
 59 ctgatgtatt gtaggacttt cagccatttg tccttgatca tgcctgggc ttttaacaac 960  
 61 atcaagagac ttagtgaaca ttactctta cccatatgtt ggtctattta ttcccagagt 1020  
 63 agaaggctct actcctcagt caggctggga actaccagg gatactccag actgccagtt 1080  
 65 tcttggtctc agaggatggc gaagtgcaca gctggacaca aacaaagggt tagtgaacac 1140  
 67 ttgctgaagt tgaagaacag aagctgagga agaggaagga tagtttcacc ccttccgtgc 1200  
 69 tcctgatagt cctcccagt gtaggacata gagactgtgg gggacaagct attgggggtg 1260  
 71 aagaaggagc aagtagatcc cagagacaca cccagtggt cctgccctga gcctgacaga 1320  
 73 gccctcttcc ctctcagca caacaaagga cacaacctta aagggtctct acatcccaaa 1380  
 76 <210> SEQ ID NO: 2  
 77 <211> LENGTH: 20

(Pg. 6)

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78 <212> TYPE: DNA
79 <213> ORGANISM: Canis familiaris
81 <400> SEQUENCE: 2
82 cctccaccat cttctgcttg                                20
85 <210> SEQ ID NO: 3
86 <211> LENGTH: 20
87 <212> TYPE: DNA
88 <213> ORGANISM: Canis familiaris
90 <400> SEQUENCE: 3
91 atgtcctgga cactgcgctc                                20
94 <210> SEQ ID NO: 4
95 <211> LENGTH: 20
96 <212> TYPE: DNA
97 <213> ORGANISM: Canis familiaris
99 <400> SEQUENCE: 4
100 tccccctcct aatgagctcc                                20
103 <210> SEQ ID NO: 5
104 <211> LENGTH: 20
105 <212> TYPE: DNA
106 <213> ORGANISM: Canis familiaris
108 <400> SEQUENCE: 5
109 gaggccatgg gtgaccccttc                                20
112 <210> SEQ ID NO: 6
113 <211> LENGTH: 20
114 <212> TYPE: DNA
115 <213> ORGANISM: Canis familiaris
117 <400> SEQUENCE: 6
118 cctccaccat cttctgcttg                                20
121 <210> SEQ ID NO: 7
122 <211> LENGTH: 20
123 <212> TYPE: DNA
124 <213> ORGANISM: Canis familiaris
126 <400> SEQUENCE: 7
127 caatgacatt ggccactgac                                20
130 <210> SEQ ID NO: 8
131 <211> LENGTH: 20
132 <212> TYPE: DNA
133 <213> ORGANISM: Canis familiaris
135 <400> SEQUENCE: 8
136 tttggggccg gatttgacac                                20
139 <210> SEQ ID NO: 9
140 <211> LENGTH: 20
141 <212> TYPE: DNA
142 <213> ORGANISM: Canis familiaris
144 <400> SEQUENCE: 9
145 gaggccatgg gtgaccccttc                                20
148 <210> SEQ ID NO: 10
149 <211> LENGTH: 18
150 <212> TYPE: DNA

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151 <213> ORGANISM: Canis familiaris
153 <400> SEQUENCE: 10
154 ctggagtctt atgtacct                                     18
157 <210> SEQ ID NO: 11
158 <211> LENGTH: 18
159 <212> TYPE: DNA
160 <213> ORGANISM: Canis familiaris
162 <400> SEQUENCE: 11
163 ccactgggttt atgaagac                                     18
166 <210> SEQ ID NO: 12
167 <211> LENGTH: 19
168 <212> TYPE: DNA
169 <213> ORGANISM: Canis familiaris
171 <400> SEQUENCE: 12
172 tgcccttaat ggaggcctt                                     19
175 <210> SEQ ID NO: 13
176 <211> LENGTH: 20
177 <212> TYPE: DNA
178 <213> ORGANISM: Canis familiaris
180 <400> SEQUENCE: 13
181 acgacacccc ctaccacttc                                     20
184 <210> SEQ ID NO: 14
185 <211> LENGTH: 20
186 <212> TYPE: DNA
187 <213> ORGANISM: Canis familiaris
189 <400> SEQUENCE: 14
190 ttcatacttg agatcttccg                                     20
193 <210> SEQ ID NO: 15
194 <211> LENGTH: 20
195 <212> TYPE: DNA
196 <213> ORGANISM: Canis familiaris
198 <400> SEQUENCE: 15
199 aattggaggt tgaccgcatc                                     20
202 <210> SEQ ID NO: 16
203 <211> LENGTH: 20
204 <212> TYPE: DNA
205 <213> ORGANISM: Canis familiaris
207 <400> SEQUENCE: 16
208 ttcatacttg agatcttctg                                     20
211 <210> SEQ ID NO: 17
212 <211> LENGTH: 20
213 <212> TYPE: DNA
214 <213> ORGANISM: Canis familiaris
216 <400> SEQUENCE: 17
217 cccggttttg tcttctgtgt                                     20
220 <210> SEQ ID NO: 18
221 <211> LENGTH: 20
222 <212> TYPE: DNA
223 <213> ORGANISM: Canis familiaris

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```

225 <400> SEQUENCE: 18
226 tgacgtggcc agaagtgaga                                20
229 <210> SEQ ID NO: 19
230 <211> LENGTH: 44
231 <212> TYPE: RNA
232 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
235 <223> OTHER INFORMATION: Description of Artificial Sequence: an artificially
synthesized
236     GeneRacer RNA Oligo
238 <400> SEQUENCE: 19
239 cgacuggagc acgaggacac ugacauggac ugaaggagua gaaa        44
242 <210> SEQ ID NO: 20
243 <211> LENGTH: 23
244 <212> TYPE: DNA
245 <213> ORGANISM: Artificial Sequence
247 <220> FEATURE:
248 <223> OTHER INFORMATION: Description of Artificial Sequence: an artificially
synthesized
249     GeneRacer 5' primer
251 <400> SEQUENCE: 20
252 cgactggagc acgaggacac tga                                23
255 <210> SEQ ID NO: 21
256 <211> LENGTH: 24
257 <212> TYPE: DNA
258 <213> ORGANISM: Canis familiaris
260 <400> SEQUENCE: 21
261 ggactcttca ggcctttggg aagc                                24
264 <210> SEQ ID NO: 22
265 <211> LENGTH: 1638
266 <212> TYPE: DNA
267 <213> ORGANISM: Canis familiaris
269 <220> FEATURE:
270 <221> NAME/KEY: CDS
271 <222> LOCATION: (63)..(1601)
272 <223> OTHER INFORMATION:
W--> 275 <400> 22
276 agctctgtac cagcctccac aatcctactg atctcaagct cctgcctcta cagttgatac        60
278 ag atg gca ttg tcc cag atg gcc aca gag ctt ctc ctg gcc tcc acc        107
279     Met Ala Leu Ser Gln Met Ala Thr Glu Leu Leu Leu Ala Ser Thr
280     1         5         10        15
282 atc ttc tgc ttg gta ctc tgg gtg gtc aag gcc tgg cag cct cgg ctt        155
283 Ile Phe Cys Leu Val Leu Trp Val Val Lys Ala Trp Gln Pro Arg Leu
284         20        25        30
286 ccc aaa ggc ctg aag agt cca ccg ggg ccc tgg ggc tgg ccc ctg ctc        203
287 Pro Lys Gly Leu Lys Ser Pro Pro Gly Pro Trp Gly Trp Pro Leu Leu
288         35        40        45
290 ggg aac gtg ctg acc ttg ggc aag agc ccc cac ctg gcg ctg tcc agg        251
291 Gly Asn Val Leu Thr Leu Gly Lys Ser Pro His Leu Ala Leu Ser Arg
292         50        55        60
294 ctg agc cag cgt tat ggg gac gtg ctg cag atc cgc atc ggc tcc acc        299

```

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295	Leu	Ser	Gln	Arg	Tyr	Gly	Asp	Val	Leu	Gln	Ile	Arg	Ile	Gly	Ser	Thr	
296	65					70				75							
298	ccc	gtg	ctg	gtg	ctc	agt	ggc	ctg	gac	acc	atc	cgg	cag	gcc	ctg	gtg	347
299	Pro	Val	Leu	Val	Leu	Ser	Gly	Leu	Asp	Thr	Ile	Arg	Gln	Ala	Leu	Val	
300	80					85				90					95		
302	cgc	cag	ggg	gat	gat	ttc	aag	ggc	cgg	ccc	gac	ctc	tac	agc	ttc	tct	395
303	Arg	Gln	Gly	Asp	Asp	Phe	Lys	Gly	Arg	Pro	Asp	Leu	Tyr	Ser	Phe	Ser	
304					100					105					110		
306	ctg	gtg	acc	gac	ggc	caa	agc	ctg	acc	ttc	agc	cca	gac	tcc	gga	cca	443
307	Leu	Val	Thr	Asp	Gly	Gln	Ser	Leu	Thr	Phe	Ser	Pro	Asp	Ser	Gly	Pro	
308					115					120					125		
310	gtg	tgg	gct	gcg	cgc	agg	cgc	ctg	gct	cag	aac	gcg	ctc	aac	acc	ttc	491
311	Val	Trp	Ala	Ala	Arg	Arg	Arg	Leu	Ala	Gln	Asn	Ala	Leu	Asn	Thr	Phe	
312					130					135					140		
314	tcc	att	gcc	tcc	gac	ccg	gct	tcc	tcg	tgc	tct	tgc	tac	ctg	gaa	gag	539
315	Ser	Ile	Ala	Ser	Asp	Pro	Ala	Ser	Ser	Cys	Ser	Cys	Tyr	Leu	Glu	Glu	
316	145					150				155							
318	cat	gtg	agc	aag	gag	gcc	gag	gcc	ctt	ctc	agc	agg	ctg	cag	gag	cag	587
319	His	Val	Ser	Lys	Glu	Ala	Glu	Ala	Leu	Leu	Ser	Arg	Leu	Gln	Glu	Gln	
320	160					165				170					175		
322	atg	gca	gag	gtt	ggg	cgc	ttt	gat	ccc	tac	aac	caa	gtg	ctg	atg	tca	635
323	Met	Ala	Glu	Val	Gly	Arg	Phe	Asp	Pro	Tyr	Asn	Gln	Val	Leu	Met	Ser	
324					180					185					190		
326	gtg	gcc	aat	gtc	att	ggt	gca	atg	tgc	ttt	ggg	cac	cac	ttc	tct	cag	683
327	Val	Ala	Asn	Val	Ile	Gly	Ala	Met	Cys	Phe	Gly	His	His	Phe	Ser	Gln	
328					195					200					205		
330	aga	agt	gag	gaa	atg	ctc	ccc	ctc	cta	atg	agc	tcc	agt	gat	ttt	gtg	731
331	Arg	Ser	Glu	Glu	Met	Leu	Pro	Leu	Leu	Met	Ser	Ser	Ser	Asp	Phe	Val	
332					210					215					220		
334	gag	acc	gtc	tcc	aac	ggg	aac	ccg	gtg	gac	ttt	ttc	ccc	att	ctc	caa	779
335	Glu	Thr	Val	Ser	Asn	Gly	Asn	Pro	Val	Asp	Phe	Phe	Pro	Ile	Leu	Gln	
336	225					230				235							
338	tat	atg	ccc	aac	tca	gcc	ctg	cag	aga	ttc	aag	aac	ttc	aac	cag	acg	827
339	Tyr	Met	Pro	Asn	Ser	Ala	Leu	Gln	Arg	Phe	Lys	Asn	Phe	Asn	Gln	Thr	
340	240					245				250					255		
342	ttc	gtg	cag	tcc	ctg	cag	aaa	att	gtc	cag	gaa	cac	tat	caa	gac	ttt	875
343	Phe	Val	Gln	Ser	Leu	Gln	Lys	Ile	Val	Gln	Glu	His	Tyr	Gln	Asp	Phe	
344					260					265					270		
346	gat	gag	cgc	agt	gtc	cag	gac	atc	aca	ggc	gcc	ctc	ttg	aag	cac	aat	923
347	Asp	Glu	Arg	Ser	Val	Gln	Asp	Ile	Thr	Gly	Ala	Leu	Leu	Lys	His	Asn	
348					275					280					285		
350	gag	aag	agc	tcc	agg	gct	agt	gat	ggc	cac	atc	ccc	caa	gag	aag	att	971
351	Glu	Lys	Ser	Ser	Arg	Ala	Ser	Asp	Gly	His	Ile	Pro	Gln	Glu	Lys	Ile	
352					290					295					300		
354	gtc	aac	ctt	atc	aac	gac	att	ttt	ggg	gcc	gga	ttt	gac	act	gtc	aca	1019
355	Val	Asn	Leu	Ile	Asn	Asp	Ile	Phe	Gly	Ala	Gly	Phe	Asp	Thr	Val	Thr	
356	305					310				315							
358	acg	gcc	att	tcc	tgg	agt	ctt	atg	tac	ctt	gtg	gca	aac	cct	gag	ata	1067
359	Thr	Ala	Ile	Ser	Trp	Ser	Leu	Met	Tyr	Leu	Val	Ala	Asn	Pro	Glu	Ile	

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/536,809

DATE: 06/07/2005  
TIME: 11:17:12

Input Set : A:\08959.0011 Sequence Listing.txt  
Output Set: N:\CRF4\06072005\J536809.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:22; Xaa Pos. 415,433,435

Seq#:23; Xaa Pos. 415,433,435

## VERIFICATION SUMMARY

DATE: 06/07/2005

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TIME: 11:17:12

Input Set : A:\08959.0011 Sequence Listing.txt

Output Set: N:\CRF4\06072005\J536809.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No  
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:275 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:22,Line#:272  
L:379 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:1307  
M:341 Repeated in SeqNo=22  
L:533 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:400  
M:341 Repeated in SeqNo=23